

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Wei-Kung Wang  
Serial No. : 10/085,944  
Filed : February 28, 2002  
Title : DETECTION OF DENGUE VIRUS

Art Unit : 1645  
Examiner : Jeffrey S. Parkin

**Mail Stop Amendment**

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

REPLY TO THE NOTICE TO COMPLY WITH THE REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES MAILED DECEMBER 16, 2004

In reply to the communication mailed on December 16, 2004, enclosing a Notice to Comply with the Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures (Notice to Comply), Applicant respectfully requests reconsideration and withdrawal of the Notice to Comply, as it appears to have been sent in error.

As an initial matter, Applicant would like to thank Examiner Jeffrey S. Parkin for conducting a telephonic conference with Applicant's representative on January 5, 2005. During the conference, Applicant's representative and Examiner Parkin discussed and reached agreement on the following points:

(i) the allegedly non-compliant sequences forwarded with the Notice to Comply (i.e., Appendix A, pp. 100-104) do not belong to the specification under examination.

(ii) the allegedly non-compliant sequences, in fact, belong to prior art application WO 96/40933 (Bhamarapravati et al.), which was cited in the Office Action, mailed June 24, 2004, and in the Interview Summary form PTOL-413, mailed August 24, 2004.

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

January 18, 2005  
Date of Deposit

Linda M. White  
Signature

Linda M. White

Typed or Printed Name of Person Signing Certificate

(iii) the specification under examination discloses two nucleotide sequences, designated SEQ ID NOs 1 and 2.

During the telephonic conference, Examiner Parkin also indicated that he would try to review the pending claims before the due date for responding to the Notice to Comply and, if possible, issue a further action, such as a Notice of Allowance, clarifying that the Notice to Comply had been sent in error and obviating Applicant's need to respond.

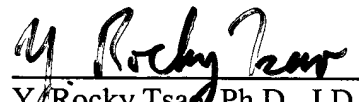
In order to avoid abandonment of the application, Applicant submits the present paper, respectfully noting that the Notice to Comply presents no reason for doubting that the present specification conforms to the requirements. Applicant further submits, after careful review of the claims and specification, that the application is in compliance with 37 C.F.R. §§ 1.821-1.825.

For the reasons presented above, Applicant respectfully (i) requests that the Examiner reconsider and withdraw the Notice to Comply, and (ii) submits that the present claims are in condition for allowance.

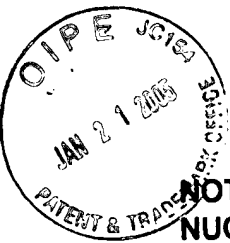
Enclosed are copies of the Notice to Comply and the allegedly non-compliant sequences (Appendix A, pp 100-104) mailed by the Office. No fee is believed to be due. Please apply any other charges or credits to deposit account 06-1050, referencing Attorney Docket No. 12563-004001.

Respectfully submitted,

Date: 1-18-05

  
Y. Rocky Tsao, Ph.D., J.D.  
Reg. No. 34,053  
Attorney for Applicant

Fish & Richardson P.C.  
225 Franklin Street  
Boston, MA 02110-2804  
Telephone: (617) 542-5070  
Facsimile: (617) 542-8906  
21011784.doc



Application No.: 10/085,944

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: see accompanying letter

**Applicant Must Provide:**

- ☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An ~~initial~~ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216  
For CRF Submission Help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

## APPENDIX A

## PRIMERS DESIGNED FOR DEN-2 CLONING/SEQUENCING PROJECT:

SEQ. ID NO.	PRIMER	LEN/SENSE	SEQUENCE
3	pUC/M13-P5	25/+	5'-CCAGTCACGACGTTGTAAAACGAC-3'
4	pUC/M13-P5B	27/+	5'-GGATGTCCTGCAAGGCGATTAACTTG-3'
5	pUC/M13-P3	25/+	5'-TGAAGGATTAACAAATTCACACAG-3'
6	pUC/M13-P3B	27/-	5'-GGCTTACACTTTATCTTCGGCTCG-3'
7	D2-1-ECD.T7 75/+		5'-GGGATATTG/GAATTC/TCGGA/ AATTTAATACACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3'  (5'-P111/EcoRI/XbaI/T7 Promoter/ 5'-end of DEN-2)
8	D2-SMT71	77/+	5'-CCAGT/GAATTC/GAGCTC/ACCGTT/ AATTTAATACACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3'  (5'-P111/EcoRI/SstI/MluI/T7 Promoter/ 5'-end of DEN-2)
9	D2-1	24/+	5'-AGTTGTTAGTCTACGTGGACCGAC-3'
10	D2-28	34/+	5'-GACAGATTCTTTGAGGGAGCTGAGCTCAACGAG-3'
11	D2-134	28/+	5'-TCATTATGCTGAACCGGAGAGAAACCG-3'
12	CD2-250	26/-	5'-GGGATTGTTAGGAAACGAGGAAACGC-3'
13	D2-274	32/+	5'-CCACCAACGACAGGATACTGAAAGATGGG-3'
14	CD2-378	25/-	5'-TGCAGATCTGGTCTCTATTCAAG-3'
15	D2-528	25/+	5'-GTGACATGTGTACCCATGCGCC-3'
16	CD2-616	26/-	5'-TTGCACCAACAGTCAATGCTTCAGG-3'
17	D2-616	25/+	5'-ACCAAGACATAGATTGTTGTC-3'
18	CD2-618	25/-	5'-GCACCAACAGTCTATGCTTCTGCG-3'
19	CD2-771	25/-	5'-ATGTTTCCAGGCCCTTCTGATGAC-3'
20	D2-847	25/+	5'-GCAGCAATCTGGCATACCATAG-3'
21	D2-996	27/+	5'-GGTTGACATAGTCTTAGACATGGAG-3'
22	CD2-996	27/-	5'-CTTCCATGTTCTAAGACTATGTCACC-3'

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SEQ. ID	PRIMER	LEN/SELEN	SEQUENCE
23	D2-1005	35/+	5'-GTCTTAAACATGGAATTTGTGTACGACGATGGC-3'
24	D2-1141	25/+	5'-ACACAGAAATCTGCTGCCAACAC-3'
25	D2-1211	25/+	5'-GCMAACACTCCATGGTAGACAGAGG-3'
26	cD2-1211	25/-	5'-CCTCTGCTACCATGGAGTGTTC-3'
27	cD2-1227	27/-	5'-CCACATCCATTTCCCATCTCTCTCT-3'
28	D2-1261	30/+	5'-GGAAAGGAGGCATTGTGACCTGTGCTATG-3'
29	D2-1416	28/+	5'-GGAAATCAAAATAACACACAGATTCC-3'
30	cD2-1503	34/-	5'-CTGCAGCAACACCATCTCAATGAGTGGAGGCC-3'
31	D2-1510	25/+	5'-GACTTCATGAGATGGTCTCTCTCC-3'
32	cD2-1510	25/+	5'-GCAGCAGCAACATCTCATGAGTC-3'
33	D2-1546	28/+	5'-AAGCTTGGCTGGTCACAGCAATGTT-3'
34	cD2-1567	27/-	5'-TGTTAAGGCAAGTCTAGAAACCATTG-3'
35	D2-1777	23/+	5'-GGACATCTCAAGTGCAGGCTGAG-3'
36	cD2-1777	23/+	5'-CTCAGCCTGCACTTGAAGATGCC-3'
37	D2-1863	27/+	5'-GAGGAATAGCAGAAACACACATGG-3'
38	cD2-1888	33/-	5'-CCCTTCAATTTGTAATCTGATAACTATTGTTCC-3'
39	D2-2047	32/+	5'-CCTCCATTCGGAGACAGCTACATCATATAGG-3'
40	cD2-2047	32/-	5'-CCTATGATGATGTAGCTGTCTCCGAATGGAGG-3'
41	D2-2170	29/+	5'-ATGGCCATTTTAAAGTGACACAGCCTGGGA-3'
42	cD2-2200	27/-	5'-TGTAACACTCTCTCCAGGGATCCAAA-3'
43	D2-2308	29/+	5'-CTCATAGGAGTCATTATCATATGATAGG-3'
44	cD2-2504	35/-	5'-GGGGAATCTGGTTGGAACTTATATTGTTCTGTCC-3'
45	cD2-2622	30/-	5'-TGATTCATTTCTGTTGTATTTGTTTCCAC-3'
46	D2-2702	25/+	5'-AAGGAATCATGCGGCAGGAAACG-3'
47	cD2-2864	22/-	5'-ACTTCCAGCGAGTTCCAGCTC-3' A A
48	D2-2992	25/+	5'-AACAGAGCCGTCCATGCGATATGG-3'
49	cD2-3105	22/-	5'-TCCATGCTCCAGAGGTGTGT-3' G
50	D2-3236	25/+	5'-AGCTTGAGATGCACTTTGATTTCTG-3'

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SEQ. ID	PRIMER	POS./SELEN	SEQUENCE
51	cD2-3410	22/-	5'-GGTCTGATTTCCATCCCTACC-3'
52	D2-3621	23/+	5'-GTCTTTAGAGACCTGGGAGAG-3'
53	cD2-3739	25/-	5'-GTTTCTCAGAGTAACTCCAGCTGC-3' C
54	D2-3905	25/+	5'-ATCAATGGCAGTGAATCATGGC-3'
55	cD2-4002	25/-	5'-TGTTAGAGCAGTGGGAAACGGAC-3' A G
56	cD2-4060	25/-	5'-GATTAGACCTTTGATGCTCAGGC-3'
57	D2-4214	25/+	5'-TGACAGACCAATTAGTGGCTGGAGG-3'
58	D2-4257	34/+	5'-GCTGCTCACTGGACGATGGCCGATTGGAACTG-3'
59	cD2-4323	24/-	5'-GGGCTGCTTCTGATATTCTGGCC-3' C
60	D2-4497	25/+	5'-CCTGTGGAGGTGAGAAACACGG-3'
61	cD2-4557	30/-	5'-GCTCACTTTCGTTTGGGCTTTCCATG-3'
62	cD2-4615	25/-	5'-CTCGGCTCCGATCTGGAGTATCC-3' G G A
63	D2-4746	25/+	5'-CCTATATCATATGGAGAGGCTGG-3'
64	D2-4792	25/+	5'-GAGGAGAGAGATCCAGGTATTGG-3'
65	cD2-4922	25/-	5'-CTGTGACAAATTGGAGATCCTGACG-3' T T
66	D2-4994	25/+	5'-GTGGGCAATGTGAGTGTATAGC-3'
67	D2-5124	25/+	5'-TCTGACTATGGCCGAGGTATCTC-3'
68	D2-5173	25/+	5'-ACATATCTTTGGCCCACTAGAG-3'
69	cD2-5272	19/-	5'-CGATCTCCGCGCGGTGTG-3' A
70	cD2-5318	25/-	5'-CTACTGGTGAAGCAGGCTCATGG-3'
71	cD2-5656	27/-	5'-CCTACTGAGTTGTATCACTTTCTTCC-3'
72	cD2-5891	26/-	5'-TGGATTCTTCTTATTTCTCCCTCTC-3'
73	D2-5770	25/+	5'-TTCAGGCTGAGAGGGTTATAGACC-3'
74	D2-6152	25/+	5'-TCTGGTTGGCTACAGATGGCAGC-3'
75	cD2-6252	27/-	5'-CCTCTTTTGTCCAGATTCTCACTCC-3' A

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SEQ. ID	PRIMER	MBR/SENSE	SEQUENCE
76	D2-6493	35/+	5'-GCTACACCATGCTCTCACTGAACTGCCGGAGAC-3'
77	cD2-6605	24/-	5'-TTCCAGGGTCATCTTCCCTATAC-3' G
78	cD2-6624	31/-	5'-GATGCTAGCCGTGATTATGACACATTCC-3'
79	D2-6748	25/+	5'-AAACAGAGAACACCCCAAGACACC-3'
80	cD2-6932	21/-	5'-CGGCATACAGCTCCATGCTG-3'
81	D2-7055	25/+	5'-GTCTCGGAAAGGATGGCCATTGTC-3'
82	cD2-7195	25/-	5'-CTCTGGTTCCTTTTGCCTGAGTCC-3' A G G
83	cD2-7217	27/-	5'-CCGCCCTGCTCTTTTCTGAGCTTCTC-3'
84	D2-7378	25/+	5'-AGGACTACATGGGCTCTGTGTGAGG-3'
85	cD2-7515	19/-	5'-GAGAGTCCAGCTCCGCC-3'
86	D2-7769	25/+	5'-AGAGAACATGGTCACACAGAGG-3'
87	cD2-7885	22/-	5'-GTCTCTGTGTCTCTGTCTCC-3'
88	D2-8165	25/+	5'-GGAAATATGGAGAGCCATGTGAGG-3'
89	cD2-8210	22/-	5'-ACCCATACATCTCATGTGTGG-3'
90	D2-8428	28/+	5'-GAGCATGAACATCATGCACTATGACC-3'
91	D2-8440	25/+	5'-TCATGGCACTATGACCAGACCC-3'
92	cD2-8529	22/-	5'-CAGTCTGACCACTCCGTTGACC-3' C A G
93	D2-8773	25/+	5'-AAGGTGAGAGCAATGCAACCTTGG-3'
94	D2-8798	29/+	5'-GGGCCAATTCAGTATGAGAACAGTGG-3'
95	cD2-8865	22/-	5'-TCTTCCCTGTCAACCACTCC-3' C T
96	D2-9046	25/+	5'-AATGAGATCACTGGTTCTCCAGG-3'
97	D2-9131	25/+	5'-AAGTGAACAAGAAAGAGGAGGAGC-3'
98	cD2-9166	22/-	5'-TGTCCATCCTGCTGTGTATC-3' A G
99	cD2-9234	30/-	5'-GCTAGTTTCTGTGTCTCTCCATGAGG-3'
100	D2-9344	25/+	5'-TCATATGAGAGAGACCAAGAGG-3'
101	cD2-9429	24/-	5'-ACTCCTTCTCCCTCCATCTGTCTG-3'

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SEQ. ID	PRIMER	SIZE/SEQUE	SEQUENCE
102	CD2-9438	27/+	5'-ATGCTTTGAGATTCCCTCTCCCTCC-3' A C
103	CD2-9468	32/-	5'-GCACAGCGATTTCCTCTGTGATTGTAGGTGC-3'
104	D2-9645	25/+	5'-ACCATGGGAACCTTCAGAGGATGG-3'
105	D2-9656.BAM	45/+	5'-TTATCACATT/GGATCC/TTCAGAGGATGGA ATGATTGGACACAG-3' (5'-P111/BamHI/DEN-2 Sequence)
106	CD2-9668	28/-	5'-CAGAGGCGCACTTGTGTCCATCATTC-3'
107	CD2-9779	21/-	5'-CTCCCTGGGAATTGGGCTC-3' T G
108	CD2-9796	28/-	5'-CGGTCTCCCGCAAGACCACTGCTCC-3'
109	CD2-9796.XBA	44/-	5'-TTATCACCTA/TCTAGA/CGGTCTCC GCAAGACCACTGCTCC-3'
110	CD2-9913	26/-	5'-GTTGGAACCCAAATGTGATGCTACTGC-3'
111	D2-9937	25/+	5'-ACCAAGTCAGCAACCTGTCATAC-3'
112	CD2-9977	21/-	5'-GCATGCTTCCCTGTCTATCC-3' T
113	CD2-10003	25/-	5'-CTTGAATCCACACCTGTTCCAGAC-3'
114	D2-10203	25/+	5'-ATACACAGATTACATGCCATCCATG-3'
115	CD2-10261	21/-	5'-TTTGGCTTCTACCAACAGAC-3' T A
116	D2-10289	25/-	5'-GAACCAAGGCTAGAGTCAGGTCCG-3'
117	CD2-10337	23/-	5'-GACGGGCTCACAGGTACATAG-3'
118	D2-10418	25/+	5'-GCTGTAGCTCCACCTGAGAGGTG-3'
119	D2-10470	25/+	5'-GGAGCTGTACGCATGCGTAGTG-3'
120	CD2-10530	19/-	5'-GGGCCCCGTGTGTCTGC-3' A
121	CD2-10687	59/-	5'-AGAACCTGTTGATTCAACAGCAACCATTCATTTCG-3'
122	CD2-10687.XBA	59/-	5'-TTATCACCTA/GCATGC/TCTAGA/ AGAACCTGTTGATTCAACAGCAACCATTCATTTCG-3' (5'-P111/SphI/XbaI/ 3'-End DEN-2 Sequence)
123	CD2-10687.X2	52/-	5'-TTATCACCTA/TCTAGA/ GAACCTGTTGATTCAACAGCAACCATTCATTTCG-3' (5'-P111/XbaI/ 3'-End DEN-2 Sequence)